Amendments to the Claims:

This listing of claims will replace all prior versions, and listings, of claims in the application:

Listing of Claims:

1. (currently amended) A method of typing a proliferative nodule in ~~a~~ congenital melanocytic nevus as a benign growth, the method comprising providing a nucleic acid sample from the nodule and detecting ~~a numerical aberration in chromosomes, wherein the numerical aberration is selected from the group consisting of a~~ gain of ~~whole chromosome 10, a gain of whole chromosome 11,~~ a loss of whole chromosome 7, ~~or a combination of these numerical aberrations,~~ thereby typing the nodule as a benign growth.

2.-4. (cancelled)

5. (previously presented) The method of claim 1, further comprising detecting a gain or loss of another whole chromosome.

6. (currently amended) The method of claim 1, wherein the detecting step comprises:

contacting a nucleic acid sample from the patient with a probe which selectively hybridizes to a target polynucleotide sequence on ~~a chromosome selected from the group consisting of chromosome 10, chromosome 11, and~~ chromosome 7; wherein the probe is contacted with the sample under conditions in which the probe binds selectively with the target polynucleotide sequence to form a stable hybridization complex;

detecting the formation of the hybridization complex; and

detecting a ~~change in chromosome number, the change selected from the group consisting of a gain of chromosome 10, a gain of chromosome 11 and~~ a loss of whole chromosome 7.

7. (previously presented) The method of claim 1, wherein the detecting step comprises an amplification reaction.

8. (previously presented) The method of claim 7, wherein the amplification reaction is a polymerase chain reaction

9. (previously presented) The method of claim 6, wherein the probe is a centromeric probe.

10. (original) The method of claim 1, wherein the nucleic acid sample is an interphase nucleus.

11. (original) The method of claim 1, wherein the nucleic acid sample is a metaphase cell.

12. (original) The method of claim 6, wherein the probe is labeled with a fluorescent label.

13. (original) The method of claim 6, wherein the probe is labeled with digoxigenin or biotin.

14. (original) The method of claim 6, further comprising the step of blocking the hybridization capacity of repetitive sequences in the nucleic acid sample.

15. (original) The method of claim 14, wherein unlabeled blocking nucleic acids comprising repetitive sequences are contacted with the sample.

16. (original) The method of claim 15, wherein the unlabeled blocking nucleic acids are Cot-1 DNA.

17. (original) The method of claim 6, wherein the probe is bound to a solid substrate.

18. (original) The method of claim 17, wherein the probe is a member of an array.

19.-20. (cancelled)